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Subject: Compliance cell size - horizontal
[Compliance Cell Size.docx](#)

FYI, here's a 2015 internal discussion paper we used to determine the horizontal aggregating/averaging.

We chose the 303(d) grid cell option after much discussion (#3 on page 3). Our original idea of using the pycnocline for vertical averaging as described in this paper didn't pan out. Thus we went with the approach we discussed yesterday.

We also looked at the results for compliance to make sure the averaging didn't mask violations. Slide 4 of the November advisory group presentation, <http://www.ecy.wa.gov/programs/wq/tmdl/deschutes/advisorycomm/111716DAGmtgEcyUpdateAK.pdf>, showed that we weren't masking violations spatially. Slide 14 of the September presentation, <http://www.ecy.wa.gov/programs/wq/tmdl/deschutes/advisorycomm/91516DAGBuddInletModelUpdate.pdf>, showed us that we weren't masking the magnitude of the violations.

We fully understand EAP's comment to provide a justification/explanation – including a biological discussion – for any aggregating/averaging of model cells, and we should be able to do that in the TMDL.

Chris, Ben, and Laurie, I want to thank you for your willingness to be engaged in this project up front. I think it will be much more constructive to have these conversations now rather than after we've submitted the TMDL. I realize that this is a significant workload and a pretty complex TMDL – it is appreciated.

Andrew

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